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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/919,932DATE: 11/26/2001
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3 <110> APPLICANT: MOECKEL, BETTINA
4 PFEFFERLE, WALTER
5 HUTHMACHER, KLAUS
6 RUECKERT, CHRISTIAN
7 KALINOWSKI, JOERN
8 PUEHLER, ALFRED
9 BINDER, MICHAEL
10 GREISSINGER, DIETER
11 THIERBACH, GEORG
13 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METY GENE
15 <130> FILE REFERENCE: 211707US0X
17 <140> CURRENT APPLICATION NUMBER: 09/919,932
18 <141> CURRENT FILING DATE: 2001-08-02
20 <150> PRIOR APPLICATION NUMBER: DE 10043334.0
21 <151> PRIOR FILING DATE: 2000-09-02
23 <150> PRIOR APPLICATION NUMBER: DE 10109690.9
24 <151> PRIOR FILING DATE: 2001-02-28
26 <150> PRIOR APPLICATION NUMBER: US 60/294,252
27 <151> PRIOR FILING DATE: 2001-05-31
29 <160> NUMBER OF SEQ ID NOS: 2
31 <170> SOFTWARE: PatentIn version 3.1
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 1720
35 <212> TYPE: DNA
36 <213> ORGANISM: Corynebacterium glutamicum
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (200)..(1510)
41 <223> OTHER INFORMATION:
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49 gtctattgca atagaccaag ctgttcagta ggggtcatgg gagaagaatt tcctaataaa      180
51 aactettaag gacotccaa atg cca aag tac gac aat tcc aat gct gac cag      232
52 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln
53 1 5 10
55 tgg ggc ttt gaa acc cgc tcc att cac gca ggc cag tca gta gac gca      280
56 Trp Gly Phe Glu Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala
57 15 20 25
59 cag acc agc gca cga aac ctt cgg atc tac caa tcc acc gct ttc gtg      328
60 Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val
61 30 35 40
63 ttc gac tcc gct gag cac gcc aag cag cgt ttc gca ctt gag gat cta      376
64 Phe Asp Ser Ala Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu
65 45 50 55
67 ggc cct gtt tac tcc cgc ctc acc aac cca acc gtt gag gct ttg gaa      424
68 Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu

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69	60	65	70	75	
71	aac cgc atc gct tcc ctc gaa ggt ggc gtc cac gct gta gcg ttc tcc	472			
72	Asn Arg Ile Ala Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser				
73	80	85	90		
75	tcc gga cag gcc gca acc acc aac gcc att ttg aac ctg gca gga gcg	520			
76	Ser Gly Gln Ala Ala Thr Thr Asn Ala ile Leu Asn Leu Ala Gly Ala				
77	95	100	105		
79	ggc gac cac atc gtc acc tcc cca cgc ctc tac ggt ggc acc gag act	568			
80	Gly Asp His ile Val Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr				
81	110	115	120		
83	cta ttc ctt atc act ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg	616			
84	Leu Phe Leu ile Thr Leu Asn Arg Leu Gly ile Asp Val Ser Phe Val				
85	125	130	135		
87	gaa aac ccc gac gac cct gag tcc tgg cag gca gcc gtt cag cca aac	664			
88	Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn				
89	140	145	150	155	
91	acc aaa gca ttc ttc ggc gag act ttc gcc aac cca cag gca gac gtc	712			
92	Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val				
93	160	165	170		
95	ctg gat att cct gcg gtg gct gaa gtt gcg cac cgc aac agc gtt cca	760			
96	Leu Asp ile Pro Ala Val Ala Glu Val Ala His Arg Asn Ser Val Pro				
97	175	180	185		
99	ctg atc atc gac aac acc atc gct acc gca gcg ctc gtg cgc ccg ctc	808			
100	Leu ile ile Asp Asn Thr ile Ala Thr Ala Ala Leu Val Arg Pro Leu				
101	190	195	200		
103	gag ctc ggc gca gac gtt gtc gtc gct tcc ctc acc aag ttc tac acc	856			
104	Glu Leu Gly Ala Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr				
105	205	210	215		
107	ggc aac ggc tcc gga ctg ggc ggc gtg ctt atc gac ggc gga aag ttc	904			
108	Gly Asn Gly Ser Gly Leu Gly Gly Val Leu ile Asp Gly Gly Lys Phe				
109	220	225	230	235	
111	gat tgg act gtc gaa aag gat gga aag cca gta ttc ccc tac ttc gtc	952			
112	Asp Trp Thr Val Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val				
113	240	245	250		
115	act cca gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca	1000			
116	Thr Pro Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala				
117	255	260	265		
119	cca gcc ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc	1048			
120	Pro Ala Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly				
121	270	275	280		
123	tcc acc ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac	1096			
124	Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly ile Asp				
125	285	290	295		
127	acc ctt tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt	1144			
128	Thr Leu Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala ile Lys Val				
129	300	305	310	315	
131	gca gaa ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca	1192			
132	Ala Glu Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala				
133	320	325	330		

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135 ggc ctg aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg      1240
136 Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu
137          335          340          345
139 aag tac acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat      1288
140 Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp
141          350          355          360
143 gag gct tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca      1336
144 Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala
145          365          370          375
147 aac atc ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc      1384
148 Asn Ile Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr
149          380          385          390          395
151 cat tca cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag      1432
152 His Ser Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln
153          400          405          410
155 tcc acc gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc      1480
156 Ser Thr Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile
157          415          420          425
159 gct gac ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc      1530
160 Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
161          430          435
163 ccagtgctta aagcgctggg tttttctttt tcagactcgt gagaatgcaa actagactag      1590
165 acagagctgt ccatatacac tggacgaagt tttagtcttg tccacccaga acaggcggtt      1650
167 attttcatgc ccaccttcgc gccttcaggt caacttgaaa tccaagcgat cggtgatgct      1710
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173 <211> LENGTH: 437
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175 <213> ORGANISM: Corynebacterium glutamicum
177 <400> SEQUENCE: 2
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187 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
188          35          40          45
191 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
192          50          55          60
195 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
196 65          70          75          80
199 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
200          85          90          95
203 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
204          100          105          110
207 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
208          115          120          125
211 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
212          130          135          140
215 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe

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216	145				150				155			160				
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220					165				170						175	
223	Val	Ala	Glu	Val	Ala	His	Arg	Asn	Ser	Val	Pro	Leu	Ile	Ile	Asp	Asn
224					180				185						190	
227	Thr	Ile	Ala	Thr	Ala	Ala	Leu	Val	Arg	Pro	Leu	Glu	Leu	Gly	Ala	Asp
228					195				200					205		
231	Val	Val	Val	Ala	Ser	Leu	Thr	Lys	Phe	Tyr	Thr	Gly	Asn	Gly	Ser	Gly
232					210				215					220		
235	Leu	Gly	Gly	Val	Leu	Ile	Asp	Gly	Gly	Lys	Phe	Asp	Trp	Thr	Val	Glu
236	225								230					235		240
239	Lys	Asp	Gly	Lys	Pro	Val	Phe	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala
240					245					250				255		
243	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu
244					260				265					270		
247	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala
248					275				280					285		
251	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg
252					290				295					300		
255	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn
256	305					310				315					320	
259	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser
260					325					330				335		
263	Pro	Trp	Tyr	Ala	Thr	Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr	Thr	Gly	Ser
264					340				345					350		
267	Val	Leu	Thr	Phe	Glu	Ile	Lys	Gly	Gly	Lys	Asp	Glu	Ala	Trp	Ala	Phe
268					355				360					365		
271	Ile	Asp	Ala	Leu	Lys	Leu	His	Ser	Asn	Leu	Ala	Asn	Ile	Gly	Asp	Val
272					370				375					380		
275	Arg	Ser	Leu	Val	Val	His	Pro	Ala	Thr	Thr	Thr	His	Ser	Gln	Ser	Asp
276	385					390				395					400	
279	Glu	Ala	Gly	Leu	Ala	Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr	Val	Arg	Leu
280					405				410					415		
283	Ser	Val	Gly	Ile	Glu	Thr	Ile	Asp	Asp	Ile	Ile	Ala	Asp	Leu	Glu	Gly
284					420				425					430		
287	Gly	Phe	Ala	Ala	Ile											
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VERIFICATION SUMMARY

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